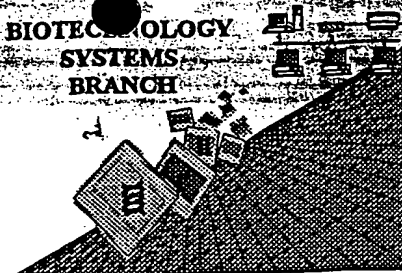




## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/836,911  
Source: OIPE  
Date Processed by STIC: 5/3/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

Does Not Comply  
Corrected Diskette Needed

PS

## SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: Hadlaczky, Gyula  
7 Szalay, Aladar  
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES  
12 (iii) NUMBER OF SEQUENCES: 34  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe  
16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor  
17 (C) CITY: San Diego  
18 (D) STATE: CA  
19 (E) COUNTRY: USA  
20 (F) ZIP: 92122  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Diskette  
24 (B) COMPUTER: IBM Compatible  
25 (C) OPERATING SYSTEM: DOS  
26 (D) SOFTWARE: FastSEQ Version 1.5  
28 (vi) CURRENT APPLICATION DATA:  
C--> 29 (A) APPLICATION NUMBER: US/09/836,911  
C--> 30 (B) FILING DATE: 17-Apr-2001  
50 (C) CLASSIFICATION:  
C--> 47 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: 08/835,682  
34 (B) FILING DATE: 10-APR-1997  
38 (A) APPLICATION NUMBER: 08/695,191  
39 (B) FILING DATE: 07-AUG-1996  
43 (A) APPLICATION NUMBER: 08/682,080  
44 (B) FILING DATE: 15-JUL-1996  
48 (A) APPLICATION NUMBER: 08/629,822  
49 (B) FILING DATE: 10-APR-1996  
52 (viii) ATTORNEY/AGENT INFORMATION:  
53 (A) NAME: Seidman, Stephanie L  
54 (B) REGISTRATION NUMBER: 33,779  
55 (C) REFERENCE/DOCKET NUMBER: 24601-402I  
58 (ix) TELECOMMUNICATION INFORMATION:  
59 (A) TELEPHONE: 858-450-8403  
60 (B) TELEFAX: 858-587-5360  
61 (C) TELEX:  
63 (2) INFORMATION FOR SEQ ID NO: 1:  
65 (i) SEQUENCE CHARACTERISTICS:  
66 (A) LENGTH: 1293 base pairs  
67 (B) TYPE: nucleic acid  
68 (C) STRANDEDNESS: single  
69 (D) TOPOLOGY: linear  
71 (ii) MOLECULE TYPE: Genomic DNA

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
 TIME: 15:56:14

Input Set : A:\4021seq.001  
 Output Set: N:\CRF3\05032001\I836911.raw

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72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
76      (ix) FEATURE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80  GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT      60
81  TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTNACAGTT TTNCAGTGAT      120
82  TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN      180
83  GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCTCTC      240
84  GCCATATTTT ACGTCTCAAA ATGTGTATTT CTCGTTTNCG GTGATTTTCA GTTTTCTCGC      300
85  CAGATTCAGG GTCCTATAAT GTGCATTTCT CATTNNCAC GTTTTTCAGT GATTTTCGTCA      360
86  TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
87  ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT      480
88  TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTCTC CGCCATATTC      540
89  CAGGTCCTAC AGTGTGCATT CCTCATTTTTC CACCTTTTTC ACTGATTTTCG TCATTTTTC      600
90  AGTCGTCAAC TGGATCTTTT TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG      660
91  TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG      720
92  TGCTAAAGTG TGTATTCTT ATTTCCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
93  CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTTCGTCATT TTTTCCAGTT      840
94  GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTT CTTGCTATAT TCCATGTCCT      900
95  ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTC TCACCATATT TCACGTCCTA      960
96  AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCTCT GCCATATTCC AGGTCCTACA      1020
97  GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAAATTTCTT CATTTTAA GGCCTCAAAT      1080
98  GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
99  ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTTCATCGG ACATTTACAG TCCTAAAGTG      1200
100  TGTATTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
101  CATTTCTCAT TTTTACGTT TTTTCAGTGA TTC      1293
103  (2) INFORMATION FOR SEQ ID NO: 2:
105      (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 1044 base pairs
107          (B) TYPE: nucleic acid
108          (C) STRANDEDNESS: single
109          (D) TOPOLOGY: linear
111      (ii) MOLECULE TYPE: Genomic DNA
112      (iii) HYPOTHETICAL: NO
C--> 113      (iv) ANTI-SENSE: NO
W--> 114      (v) FRAGMENT TYPE:
115      (vi) ORIGINAL SOURCE:
116      (ix) FEATURE:
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120  AGGCCTATGG TGAAAAAGGA AATATCTTCC CTGAAAACT AGACAGAAGG ATTCTCAGAA      60
121  TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTTT GATAGAGCAG      120
122  TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTT      180
123  CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240
124  TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA      300
125  ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTGAGAG GATCTCAGGA CTGCGGTGAA      360
126  AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT      420
127  GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT      480

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:14

Input Set : A:\402iseq.001

Output Set: N:\CRF3\05032001\I836911.raw

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128 TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCTGTTGG GAAACGGGAT 540
129 TACATATAAA AAGCAGACAG CAGCATTTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG 600
130 TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT 660
131 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
132 AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT 780
133 GAAGCTTTCT TTTGATAGAG GCAGTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
134 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
135 CATTCCCAGA ATCTGTTTGT TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT 960
136 CAGAGAGCAG GTTTGAACAC TCTTTTATA GTATCTGGAT GTGGACATT GGAGCGCTTT 1020
137 CAGGGGGGAT CCTCTAGAAT TCCT 1044

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141 (2) INFORMATION FOR SEQ ID NO: 3:

143 (i) SEQUENCE CHARACTERISTICS:

144 (A) LENGTH: 2492 base pairs

145 (B) TYPE: nucleic acid

146 (C) STRANDEDNESS: single

147 (D) TOPOLOGY: linear

149 (ii) MOLECULE TYPE: Genomic DNA

150 (iii) HYPOTHETICAL: NO

C--&gt; 151 (iv) ANTI-SENSE: NO

W--&gt; 152 (v) FRAGMENT TYPE:

153 (vi) ORIGINAL SOURCE:

154 (ix) FEATURE:

156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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158 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCTTACT ACTCAGATGG GGTGGCCGAG 60
159 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
160 GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
161 GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
162 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
163 TGCTATCCTG GGGTTCAACC CCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
164 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG 420
165 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
166 AGGGCCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
167 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
168 TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
169 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
170 GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
171 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
172 GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
173 AGAGTTCTTG TTTTCTCTTC AGCAATTTGT CATTTTAAA AGAGTTTAGC AATTCTAACA 960
174 GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
175 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
176 CATTTCTTGN NTTTTNGGCTG TTTAATTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
177 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
178 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
179 TTTTGTGTAT ATCTACCTTT TGTGTCAATT GTTAAATTC ATTACCAAC CCAAAGGCAG 1320
180 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCAATT TTAGTGTAAG 1380
181 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTT CGTCTATATC CATATCATTT 1440
182 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
183 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GCCTCCTGG AAAAGGGAAA 1560

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:14

Input Set : A:\4021seq.001

Output Set: N:\CRF3\05032001\I836911.raw

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184 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
185 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
186 GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA 1740
187 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
188 CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAGA GGCAGGCGCA GTAGGTACAA 1860
189 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
190 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
191 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
192 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGA CTCTTAG 2100
193 GCTGTTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
194 CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGA AAATGTT 2220
195 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
196 TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
197 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
198 CCTCGACACT GACAGCAATA GGTCCCGGCA GTGTCCCGAG CTGCCAGCAG GGGGCGTACG 2460
199 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

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## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:14

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

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245      (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
248      (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250      (v) FRAGMENT TYPE:
251      (vi) ORIGINAL SOURCE:
252      (ix) FEATURE:
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC 47
260 (2) INFORMATION FOR SEQ ID NO: 7:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 25 base pairs
264          (B) TYPE: nucleic acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
268      (ii) MOLECULE TYPE: Genomic DNA
269      (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271      (v) FRAGMENT TYPE:
272      (vi) ORIGINAL SOURCE:
273      (ix) FEATURE:
275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTTAAAT TAATTAAGCC CGGGC 25
280 (2) INFORMATION FOR SEQ ID NO: 8:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 27 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: single
286          (D) TOPOLOGY: linear
288      (ii) MOLECULE TYPE: Genomic DNA
289      (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291      (v) FRAGMENT TYPE:
292      (vi) ORIGINAL SOURCE:
293      (ix) FEATURE:
295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTTAAT TAATTCGGGC CCGTCGA 27
299 (2) INFORMATION FOR SEQ ID NO: 9:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 69 base pairs
303          (B) TYPE: nucleic acid
304          (C) STRANDEDNESS: single
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: Genomic DNA
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
W--> 315 GTC ACA AAC AGT GCA CCT ACT 69
316 Val Thr Asn Ser Ala Pro Thr

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*Please edit all subsequent sequences  
containing these errors*

*(Per  
Sequence Rules  
Number  
the  
amino  
acids  
under every  
5 amino  
acids — do not  
use TAB codes  
between numbers 5/3/01*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

TIME: 15:56:15

Input Set : A:\4021seq.001

Output Set: N:\CRF3\05032001\I836911.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1  
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1  
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2  
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2  
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3  
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3  
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4  
L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4  
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L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5  
L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5  
L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6  
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7  
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8  
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:  
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]  
L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11  
L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11  
L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12  
L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12  
L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13  
L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14  
L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001  
TIME: 15:56:15

Input Set : A:\402iseq.001  
Output Set: N:\CRF3\05032001\I836911.raw

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L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17  
L:1713 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1714 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18  
L:1734 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19  
L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20  
L:1789 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21  
L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22  
L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23  
L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24  
L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25  
L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26  
L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27  
L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28  
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29  
L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30  
L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31  
L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32  
L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33  
L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34